

1638

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/435,054

DATE: 08/07/2001

TIME: 08:22:55

Input Set : A:\0943SEQLIST.txt

Output Set: N:\CRF3\08072001\I435054.raw

P.S

ENTERED

4 <110> APPLICANT: Lowe, Keith S.
 5 Gordon-Kamm, William J.
 6 Klein, Theodore M.
 7 Rasco-Gaunt, Sonriza
 8 Cahoon, Rebecca E.
 9 Sun, Xifan
 10 Hoester, George J.
 11 Gregory, Carolyn A.
 12 Nadimpalli, Ramgopal
 14 <120> TITLE OF INVENTION: Transcriptional Activator Nucleic Acids,
 15 Polypeptides, and Methods of Use Thereof
 18 <130> FILE REFERENCE: 0943
 20 <140> CURRENT APPLICATION NUMBER: 09/435,054
 21 <141> CURRENT FILING DATE: 1999-11-08
 23 <150> PRIOR APPLICATION NUMBER: 60/107,643
 24 <151> PRIOR FILING DATE: 1998-11-09
 26 <160> NUMBER OF SEQ ID NOS: 23
 28 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 30 <210> SEQ ID NO: 1
 31 <211> LENGTH: 1173
 32 <212> TYPE: DNA
 33 <213> ORGANISM: Zea mays
 35 <220> FEATURE:
 36 <221> NAME/KEY: CDS
 37 <222> LOCATION: (69)...(902)
 39 <400> SEQUENCE: 1
 40 ccacgcgtcc gccaccacac cagagcgcg cgataaccct agctagcttc aggtagtagc 60
 41 gagagcca atg gac tcc agc agc ttc ctc cct gcc gcc ggc gcg gag aat 110
 42 Met Asp Ser Ser Ser Phe Leu Pro Ala Ala Gly Ala Glu Asn
 43 1 5 10
 45 ggc tcg gcg gcg ggc ggc gcc aac aat ggc ggc gct gct cag cag cat 158
 46 Gly Ser Ala Ala Gly Gly Ala Asn Asn Gly Gly Ala Ala Gln Gln His
 47 15 20 25 30
 49 gcg gcg ccg gcg atc cgc gag cag gac cgg ctg atg ccg atc gcg aac 206
 50 Ala Ala Pro Ala Ile Arg Glu Gln Asp Arg Leu Met Pro Ile Ala Asn
 51 35 40 45
 53 gtg atc cgc atc atg cgg cgc gtg ctg ccg gcg cac gcc aag atc tcg 254
 54 Val Ile Arg Ile Met Arg Arg Val Leu Pro Ala His Ala Lys Ile Ser
 55 50 55 60
 57 gac gac gcc aag gag acg atc cag gag tgc gtg tcg gag tac atc agc 302
 58 Asp Asp Ala Lys Glu Thr Ile Gln Glu Cys Val Ser Glu Tyr Ile Ser
 59 65 70 75
 61 ttc atc acg ggg gag gcc aac gag cgg tgc cag cgg gag cag cgc aag 350
 62 Phe Ile Thr Gly Glu Ala Asn Glu Arg Cys Gln Arg Glu Gln Arg Lys
 63 80 85 90
 65 acc atc acc gcc gag gac gtg ctg tgg gcc atg agc cgc ctc ggc ttc 398
 66 Thr Ile Thr Ala Glu Asp Val Leu Trp Ala Met Ser Arg Leu Gly Phe

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```

67   95                               100                               105                               110
69   gac gac tac gtc gag ccg ctc ggc gcc tac ctc cac cgc tac cgc gag      446
70   Asp Asp Tyr Val Glu Pro Leu Gly Ala Tyr Leu His Arg Tyr Arg Glu
71                               115                               120                               125
73   ttc gag ggc gac gcg cgc ggc gtc ggg ctc gtc ccg ggg gcc gcc cca      494
74   Phe Glu Gly Asp Ala Arg Gly Val Gly Leu Val Pro Gly Ala Ala Pro
75                               130                               135                               140
77   tcg cgc ggc ggc gac cac cac ccg cac tcc atg tcg cca gcg gcg atg      542
78   Ser Arg Gly Gly Asp His His Pro His Ser Met Ser Pro Ala Ala Met
79                               145                               150                               155
81   ctc aag tcc cgc ggg cca gtc tcc gga gcc gcc atg cta ccg cac cac      590
82   Leu Lys Ser Arg Gly Pro Val Ser Gly Ala Ala Met Leu Pro His His
83   160                               165                               170
85   cac cac cac cac gac atg cag atg cac gcc gcc atg tac ggg gga acg      638
86   His His His His Asp Met Gln Met His Ala Ala Met Tyr Gly Gly Thr
87   175                               180                               185                               190
89   gcc gtg ccc ccg ccg gcc ggg cct cct cac cac ggc ggg ttc ctc atg      686
90   Ala Val Pro Pro Pro Ala Gly Pro Pro His His Gly Gly Phe Leu Met
91                               195                               200                               205
93   cca cac cca cag ggt agt agc cac tac ctg cct tac gcg tac gag ccc      734
94   Pro His Pro Gln Gly Ser Ser His Tyr Leu Pro Tyr Ala Tyr Glu Pro
95   210                               215                               220
97   acg tac ggc ggt gag cac gcc atg gct gca tac tat gga ggc gcc gcg      782
98   Thr Tyr Gly Gly Glu His Ala Met Ala Ala Tyr Tyr Gly Gly Ala Ala
99   225                               230                               235
101  tac gcg ccc ggc aac ggc ggg agc ggc gac ggc agt ggc agt ggc gcc      830
102  Tyr Ala Pro Gly Asn Gly Gly Ser Gly Asp Gly Ser Gly Ser Gly Gly
103   240                               245                               250
105  ggt ggc ggg agc gcg tcg cac aca ccg cag ggc agc ggc ggc ttg gag      878
106  Gly Gly Gly Ser Ala Ser His Thr Pro Gln Gly Ser Gly Gly Leu Glu
107   255                               260                               265                               270
109  cac ccg cac ccg ttc gcg tac aag tagctagttc gtacgtcgtt cgacttgagc      932
110  His Pro His Pro Phe Ala Tyr Lys
111   275
113  aagccatcga tctgtgatc tgaacgtacg ctgtattgta cacgcatgca cgtacgtatc      992
114  ggcggctagc tctcctgttt aagttgtact gtgattctgt cccggccggc tagcaactta      1052
115  gtatcttcct tcagtctcta gtttcttagc agtcgtagaa gtgttcaatg cttgccagtg      1112
116  tgttgtttta gggccggggg aaaccatccg atgagattat ttcaaaaaaa aaaaaaaaaa      1172
117  a                                                                                          1173
119  <210> SEQ ID NO: 2
120  <211> LENGTH: 278
121  <212> TYPE: PRT
122  <213> ORGANISM: Zea mays
124  <400> SEQUENCE: 2
125  Met Asp Ser Ser Ser Phe Leu Pro Ala Ala Gly Ala Glu Asn Gly Ser
126   1                               5                               10                               15
127  Ala Ala Gly Gly Ala Asn Asn Gly Gly Ala Ala Gln Gln His Ala Ala
128   20                               25                               30
129  Pro Ala Ile Arg Glu Gln Asp Arg Leu Met Pro Ile Ala Asn Val Ile

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Input Set : A:\0943SEQLIST.txt

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```

130          35          40          45
131 Arg Ile Met Arg Arg Val Leu Pro Ala His Ala Lys Ile Ser Asp Asp
132          50          55          60
133 Ala Lys Glu Thr Ile Gln Glu Cys Val Ser Glu Tyr Ile Ser Phe Ile
134 65          70          75          80
135 Thr Gly Glu Ala Asn Glu Arg Cys Gln Arg Glu Gln Arg Lys Thr Ile
136          85          90          95
137 Thr Ala Glu Asp Val Leu Trp Ala Met Ser Arg Leu Gly Phe Asp Asp
138          100          105          110
139 Tyr Val Glu Pro Leu Gly Ala Tyr Leu His Arg Tyr Arg Glu Phe Glu
140          115          120          125
141 Gly Asp Ala Arg Gly Val Gly Leu Val Pro Gly Ala Ala Pro Ser Arg
142          130          135          140
143 Gly Gly Asp His His Pro His Ser Met Ser Pro Ala Ala Met Leu Lys
144 145          150          155          160
145 Ser Arg Gly Pro Val Ser Gly Ala Ala Met Leu Pro His His His His
146          165          170          175
147 His His Asp Met Gln Met His Ala Ala Met Tyr Gly Gly Thr Ala Val
148          180          185          190
149 Pro Pro Pro Ala Gly Pro Pro His His Gly Gly Phe Leu Met Pro His
150          195          200          205
151 Pro Gln Gly Ser Ser His Tyr Leu Pro Tyr Ala Tyr Glu Pro Thr Tyr
152          210          215          220
153 Gly Gly Glu His Ala Met Ala Ala Tyr Tyr Gly Gly Ala Ala Tyr Ala
154 225          230          235          240
155 Pro Gly Asn Gly Gly Ser Gly Asp Gly Ser Gly Ser Gly Gly Gly Gly
156          245          250          255
157 Gly Ser Ala Ser His Thr Pro Gln Gly Ser Gly Gly Leu Glu His Pro
158          260          265          270
159 His Pro Phe Ala Tyr Lys
160          275
162 <210> SEQ ID NO: 3
163 <211> LENGTH: 20
164 <212> TYPE: DNA
165 <213> ORGANISM: Artificial Sequence
167 <220> FEATURE:
168 <223> OTHER INFORMATION: primer
170 <400> SEQUENCE: 3
171 tagtagcgag agccaatgga
173 <210> SEQ ID NO: 4
174 <211> LENGTH: 20
175 <212> TYPE: DNA
176 <213> ORGANISM: Artificial Sequence
178 <220> FEATURE:
179 <223> OTHER INFORMATION: primer
181 <400> SEQUENCE: 4
182 gccgggacag aatcacagta
184 <210> SEQ ID NO: 5
185 <211> LENGTH: 20

```

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RAW SEQUENCE LISTING

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Input Set : A:\0943SEQLIST.txt

Output Set: N:\CRF3\08072001\I435054.raw

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186 <212> TYPE: DNA
187 <213> ORGANISM: Artificial Sequence
189 <220> FEATURE:
190 <223> OTHER INFORMATION: primer
192 <400> SEQUENCE: 5
193 tagtagcgag agccaatgga
195 <210> SEQ ID NO: 6
196 <211> LENGTH: 20
197 <212> TYPE: DNA
198 <213> ORGANISM: Artificial Sequence
200 <220> FEATURE:
201 <223> OTHER INFORMATION: primer
203 <400> SEQUENCE: 6
204 cccggcccta aaacaacaca
206 <210> SEQ ID NO: 7
207 <211> LENGTH: 481
208 <212> TYPE: DNA
209 <213> ORGANISM: Argemone mexicana
211 <220> FEATURE:
212 <221> NAME/KEY: CDS
213 <222> LOCATION: (44)...(481)
215 <221> NAME/KEY: misc_feature
216 <222> LOCATION: (1)...(481)
217 <223> OTHER INFORMATION: n = A,T,C or G
219 <400> SEQUENCE: 7
220 cgagagaaag agttggtgaa gaagaagaag aagttgaaaa gag atg gaa cgt ggt
221 Met Glu Arg Gly
222 1
224 ggt ggt ggt ggt ggt agt ggt ggt ggt ttc cat gga tat cag aaa ctc
225 Gly Gly Gly Gly Gly Ser Gly Gly Gly Phe His Gly Tyr Gln Lys Leu
226 5 10 15 20
228 cca aaa tca aac tcc gct gga atg atg ctc tcg gag cta tcg aat aac
229 Pro Lys Ser Asn Ser Ala Gly Met Met Leu Ser Glu Leu Ser Asn Asn
230 25 30 35
232 aac aac aat att gac gta aac tct aca tgt act gta cga gag caa gat
233 Asn Asn Asn Ile Asp Val Asn Ser Thr Cys Thr Val Arg Glu Gln Asp
234 40 45 50
236 cga tac atg cca att gct aat gtg atc agg atc atg cgt aag gta ctt
237 Arg Tyr Met Pro Ile Ala Asn Val Ile Arg Ile Met Arg Lys Val Leu
238 55 60 65
240 cct act cat gcc aag atc tct gac gat gcc aaa gaa act atc caa gaa
241 Pro Thr His Ala Lys Ile Ser Asp Asp Ala Lys Glu Thr Ile Gln Glu
242 70 75 80
244 tgt gtc tca gaa tac atc agt ttc atc aca agt gaa gcc aat gat cgt
245 Cys Val Ser Glu Tyr Ile Ser Phe Ile Thr Ser Glu Ala Asn Asp Arg
246 85 90 95 100
248 tgc caa cgt gaa caa aga aag aca atc aca gct gaa gat gtt tta tgg
249 Cys Gln Arg Glu Gln Arg Lys Thr Ile Thr Ala Glu Asp Val Leu Trp
250 105 110 115

```

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Input Set : A:\0943SEQLIST.txt

Output Set: N:\CRF3\08072001\I435054.raw

W--> 252 gcg atg agc aaa cta ggg ntt gat gag tac att gaa cct cta act ctt 439
 W--> 253 Ala Met Ser Lys Leu Gly Xaa Asp Glu Tyr Ile Glu Pro Leu Thr Leu
 254 120 125 130
 W--> 256 tac ctt caa cgt tat cgt gag ttt gaa ggt gna cgt tgg tca
 W--> 257 Tyr Leu Gln Arg Tyr Arg Glu Phe Glu Gly Xaa Arg Trp Ser 481
 258 135 140 145
 261 <210> SEQ ID NO: 8
 262 <211> LENGTH: 146
 263 <212> TYPE: PRT
 264 <213> ORGANISM: Argemone mexicana
 266 <220> FEATURE:
 267 <221> NAME/KEY: VARIANT
 268 <222> LOCATION: (1)...(146)
 269 <223> OTHER INFORMATION: Xaa = Any Amino Acid
 271 <400> SEQUENCE: 8
 272 Met Glu Arg Gly Gly Gly Gly Gly Ser Gly Gly Gly Phe His Gly
 273 1 5 10 15
 274 Tyr Gln Lys Leu Pro Lys Ser Asn Ser Ala Gly Met Met Leu Ser Glu
 275 20 25 30
 276 Leu Ser Asn Asn Asn Asn Asn Ile Asp Val Asn Ser Thr Cys Thr Val
 277 35 40 45
 278 Arg Glu Gln Asp Arg Tyr Met Pro Ile Ala Asn Val Ile Arg Ile Met
 279 50 55 60
 280 Arg Lys Val Leu Pro Thr His Ala Lys Ile Ser Asp Asp Ala Lys Glu
 281 65 70 75 80
 282 Thr Ile Gln Glu Cys Val Ser Glu Tyr Ile Ser Phe Ile Thr Ser Glu
 283 85 90 95
 284 Ala Asn Asp Arg Cys Gln Arg Glu Gln Arg Lys Thr Ile Thr Ala Glu
 285 100 105 110
 W--> 286 Asp Val Leu Trp Ala Met Ser Lys Leu Gly Xaa Asp Glu Tyr Ile Glu
 287 115 120 125
 W--> 288 Pro Leu Thr Leu Tyr Leu Gln Arg Tyr Arg Glu Phe Glu Gly Xaa Arg
 289 130 135 140
 290 Trp Ser
 291 145
 293 <210> SEQ ID NO: 9
 294 <211> LENGTH: 942
 295 <212> TYPE: DNA
 296 <213> ORGANISM: Glycine max
 298 <220> FEATURE:
 299 <221> NAME/KEY: CDS
 300 <222> LOCATION: (3)...(722)
 302 <400> SEQUENCE: 9
 303 gc acg agc tct ctt ata atc aca cac aca cct acc tta ata gct atg
 304 Thr Ser Ser Leu Ile Ile Thr His Thr Pro Thr Leu Ile Ala Met 47
 305 1 5 10 15
 307 gaa act gga ggc ttt cac ggc tac cgc aag ctc ccc aac acc acc gct
 308 Glu Thr Gly Gly Phe His Gly Tyr Arg Lys Leu Pro Asn Thr Thr Ala 95
 309 20 25 30

Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/435,054

DATE: 08/07/2001

TIME: 08:22:56

Input Set : A:\0943SEQLIST.txt

Output Set: N:\CRF3\08072001\I435054.raw

L:252 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:253 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:256 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:257 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:286 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:288 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:630 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:631 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:634 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:635 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:646 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:647 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:650 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:651 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:654 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:655 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:658 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:659 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:662 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:663 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:686 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:688 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:694 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:696 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:698 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:700 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:702 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:1100 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1102 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1104 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1106 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1108 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23